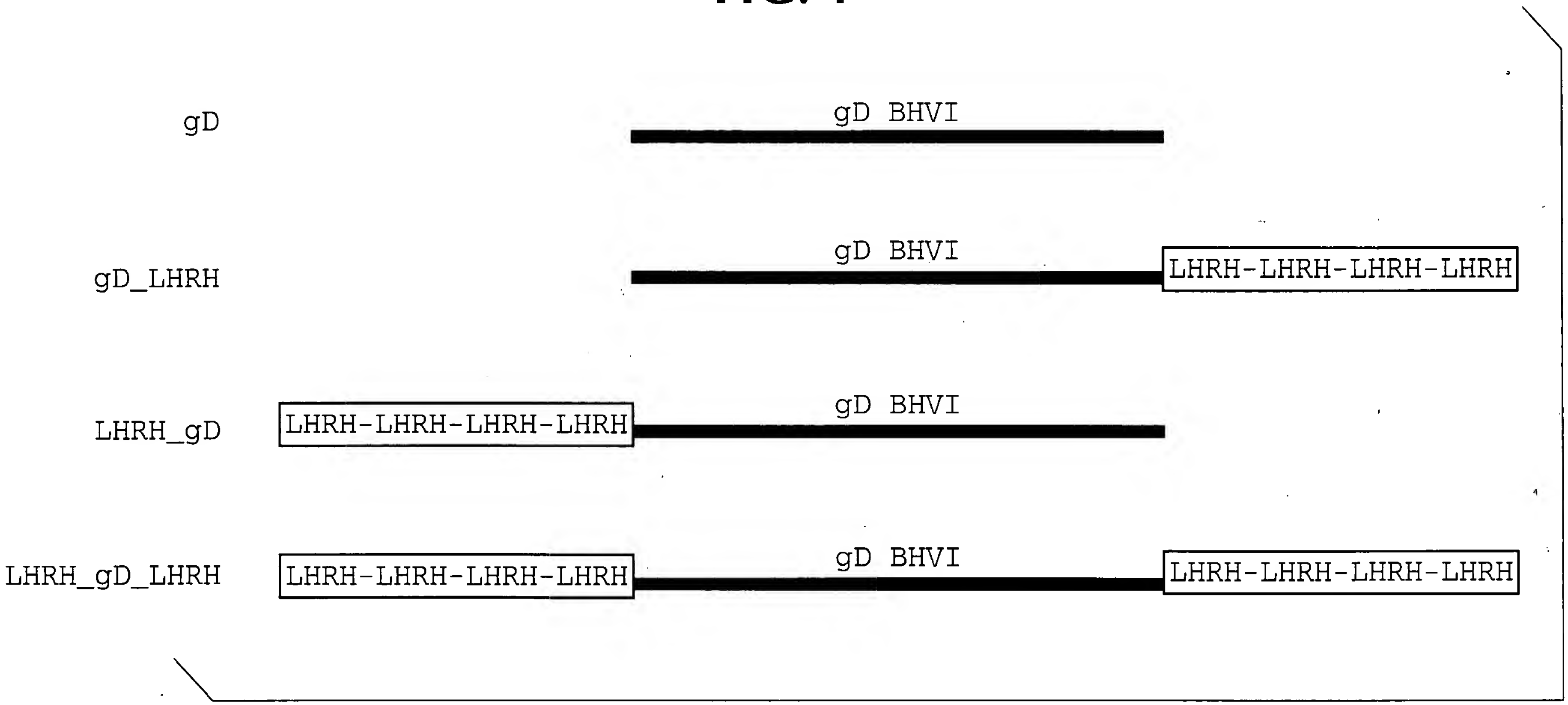
FIG. 1


gD
gD BHVI
gD_LHRH
gD BHVI
LHRH-LHRH-LHRH-LHRH
LHRH_gD
LHRH-LHRH-LHRH-LHRH
gD BHVI
LHRH_gD_LHRH
LHRH-LHRH-LHRH-LHRH
gD BHVI
LHRH-LHRH-LHRH-LHRH

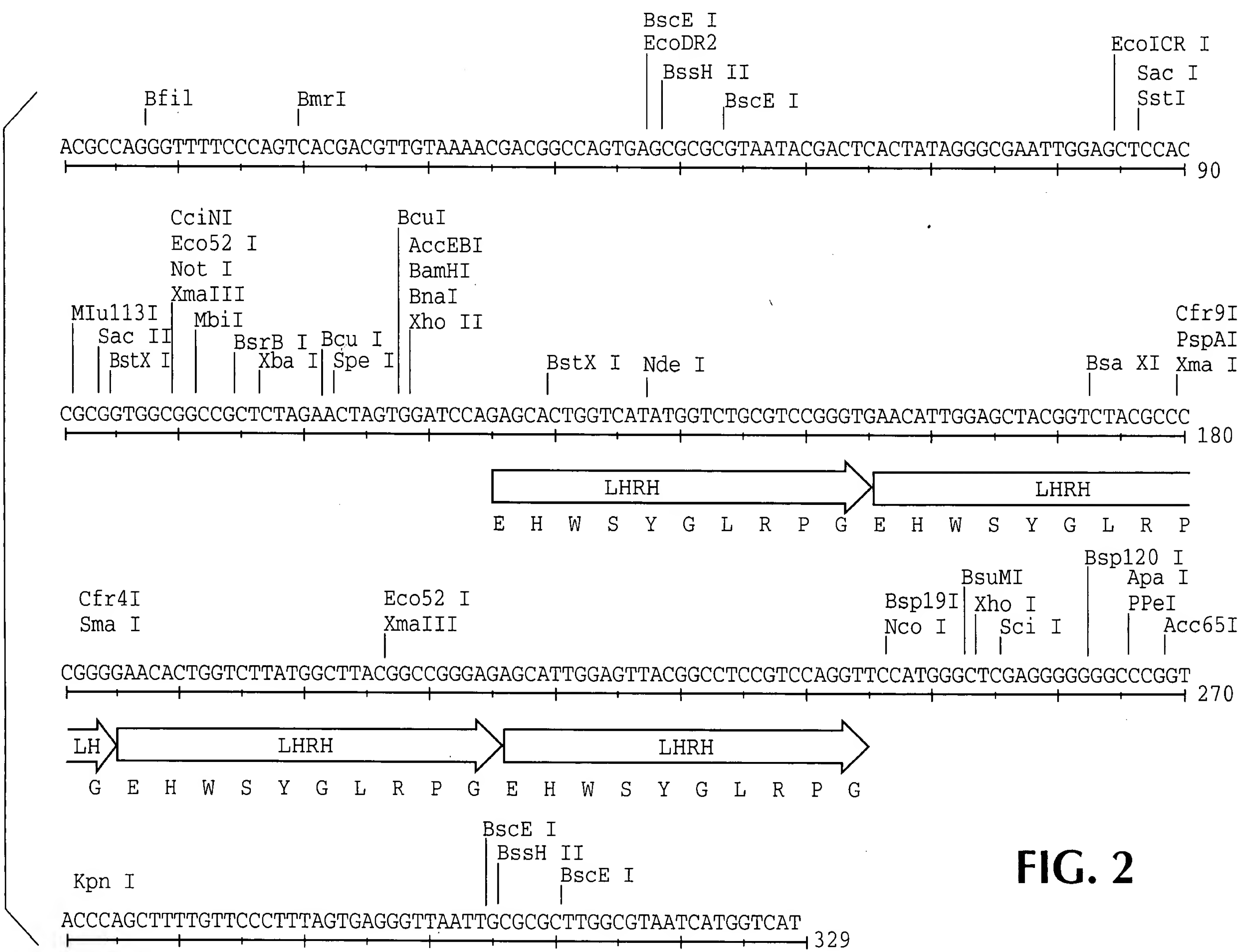

BscE I
EcoDR2
BssH II
BscE I
EcoICR I
Sac I
SstI
BfiI
BmrI
ACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAGCGCGCGTAATACGACTCACTATAGGGCGAATTGGAGCTCCAC
90
CciNI
Eco52 I
Not I
XmaIII
MIu113I
Sac II
BstX I
MbiI
BsrB I
Xba I
Bcu I
Spe I
BcuI
AccEBI
BamHI
BnaI
Xho II
BstX I
Nde I
Bsa XI
Cfr9I
PspAI
Xma I
CGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCAGAGCACTGGTCATATGGTCTGCGTCCGGGTGAACATTGGAGCTACGGTCTACGCCC
180
LHRH
LHRH
E H W S Y G L R P G E H W S Y G L R P
Cfr4I
Sma I
Eco52 I
XmaIII
Bsp19I
Nco I
BsuMI
Xho I
Sci I
Bsp120 I
Apa I
PPeI
Acc65I
CGGGGAACACTGGTCTTATGGCTTACGGCCGGGAGAGCATTGGAGTTACGGCCTCCGTCCAGGTTCCATGGGCTCGAGGGGGGGCCCGGT
270
LH
LHRH
LHRH
G E H W S Y G L R P G E H W S Y G L R P G
BscE I
BssH II
BscE I
Kpn I
ACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCAT
329

FIG. 2

FIG. 3A

CCATGGAGGGGCCGACATTGGCCGTGCTGGGCGCGCTGCTCGCCGTTGCGGTAAGCTTGCCTACACCCGCGCCGCGGGTGACGGTATACGTCGACCCGCC 100

signal sequence | Mature gD

tm_gD

Thr Met Glu Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ala Val Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro

GGCGTACCCGATGCCGCGATACAACTACACTGAACGCTGGCACACTACCGGGCCCATACCGTCGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTG 200

mature gD

tm_gD

gly **

Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val

CGCTACGCGACGAGCGCGGCGGCGTGCGACATGCTGGCGCTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACGCCGGCACGCGCGCG 300

mature gD

tm_gD

Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala Arg

CGTACAACGCCACGGTCATATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTACACCGAGTGCGAGCCCAGGAAGCACTTTGG 400

mature gD

tm_gD

gly ** **

Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys His Phe Gly

FIG. 3B

GTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGACTGATTATGGCGGCGCCCGCG 500

mature gD

tm_gD

Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro Ala

CGGCTCGTCGAGGGCCAGTACCGACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGATTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCT 600

mature gD

tm_gD

Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp Phe

CGAAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGTGCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACGTATCTCACGCAGTA 700

mature gD

tm_gD

Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu Thr Gln Tyr

CTACCCGCAGGAGGCACACAAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGTATTTTGAGGAGTCGAAGGGCTACGAGCCG 800

mature gD

tm_gD

Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro

CCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGGCAGCCGGGCGGGAGGGCA 900

mature gD

tm_gD

hydrophilic (*) charged AA

Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly

FIG. 3C

ACGGCGGCCCCCCAGGACCCGAAGGCGACGGCGAGAGTCAGACCCCCGAAGCCAACGGAGGCGCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGC 1000

mature gD

tm_gD

Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala

Xho 1 Sac 1

CGACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCACGCACCCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCCGGACGCTGTTTCGGTTTCTGTT 1100

mature gD

tm_gD

transmem

Asp Arg Pro Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg Ala Pro Asp Ala Val Ser Val Ser Val

GGTATCGGTATCGCTGCTGCTGCTATCGCTTGCGTTGCTGCTGCTGCTGGTGCTTACTTCGTTTATATTCGTCGTCGTGGTGCTGGTCCGCTGCCGC 1200

mature gD

transmembrane domain

Gly Ile Gly Ile Ala Ala Ala Ala Ile Ala Cys Val Ala Ala Ala Ala Ala Gly Ala Tyr Phe Val Tyr Ile Arg Arg Arg Gly Ala Gly Pro Leu Pro

Xba 1

GTAAACCGAAAAAACTGCCGGCTTTCGGTAACGTTAACTACAGTGCTCTGCCGGGTTGATCTAGA 1265

Mature gD

gly

Arg Lys Pro Lys Lys Leu Pro Ala Phe Gly Asn Val Asn Tyr Ser Ala Leu Pro Gly

FIG. 4A

```
                10        20        30        40
1    ATGGAGGGGCCGACATTGGCCGTGCTGGGCGCGCTGCTCG
1    ATGCAAGGGCCGACATTGGCCGTGCTGGGCGCGCTGCTCG

                50        60        70        80
41   CCGTTGCGGTAAGCTTGCCTACACCCGCGCCGCGGGTGAC
41   CCGTTGCGGTGAGCTTGCCTACACCCGCGCCGCGGGTGAC

                90       100       110       120
81   GGTATACGTCGACCCGCCGGCGTACCCGATGCCGCGATAC
81   GGTATACGTCGACCCGCCGGCGTACCCGATGCCGCGATAC

               130       140       150       160
121  AACTACACTGAACGCTGGCACACTACCGGGCCCATACCGT
121  AACTACACTGAACGCTGGCACACTACCGGGCCCATACCGT

               170       180       190       200
161  CGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTGCG
161  CGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTGCG

               210       220       230       240
201  CTACGCGACGAGCGCGGCGGCGTGCGACATGCTGGCGCTG
201  CTACGCGACGAGCGCGGCGGCGTGCGACATGCTGGCGCTG

               250       260       270       280
241  ATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGG
241  ATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGG

               290       300       310       320
281  TACGCCGGCACGCGCGCGCGTACAACGCCACGGTCATATG
281  TACGCCGGCACGCGCGCGCGTACAACGCCACGGTCATATG

               330       340       350       360
321  GTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTAC
321  GTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTAC

               370       380       390       400
361  ATGGAGTACACCGAGTGCGAGCCCAGGAAGCACTTTGGGT
361  ATGGAGTACACCGAGTGCGAGCCCAGGAAGCACTTTGGGT

               410       420       430       440
401  ACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCT
401  ACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCT
```

FIG. 4B

```
                450       460       470       480
441  GGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGACTG
441  GGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGACTG

                490       500       510       520
481  ATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACC
481  ATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACC

                530       540       550       560
521  GACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGA
521  GACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGA

                570       580       590       600
561  TTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCG
561  TTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCG

                610       620       630       640
601  AAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGTGCT
601  AAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGTGCT

                650       660       670       680
641  TCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCT
641  TCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCT

                690       700       710       720
681  GACGTATCTCACGCAGTACTACCCGCAGGAGGCACACAAG
681  GACGTATCTCACGCAGTACTACCCGCAGGAGGCACACAAG

                730       740       750       760
721  GCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCG
721  GCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCG

                770       780       790       800
761  TTCCGCCGTATTTTGAGGAGTCGAAGGGCTACGAGCCGCC
761  TTCCGCCGTATTTTGAGGAGTCGAAGGGCTACGAGCCGCC

                810       820       830       840
801  GCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGAC
801  GCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGAC

                850       860       870       880
841  GACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGG
841  GACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGG
```

FIG. 4C

```
                890       900       910       920
881   CAGCCGGGCGGGAGGGCAACGGCGGCCCCCAGGACCCGA
881   CAGCCGGGCGGGAGGGCAACGGCGGCCCCCAGGACCCGA

                930       940       950       960
921   AGGCGACGGCGAGACTCAGACCCCCGAAGCCAACGGAGGC
921   AGGCGACGGCGAGAGTCAGACCCCCGAAGCCAACGGAGGC

                970       980       990      1000
961   GCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGCCG
961   GCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGCCG

               1010      1020      1030      1040
1001  ACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCACGCA
1001  ACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCACGCA

               1050      1060      1070      1080
1041  CCCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCCGGAC
1041  CCCCCCGCCCGCCCCCGCTACGCCCGC---GGCCCCCGAC

                 →TM                  — TM —
               1090      1100      1110      1120
1081  GCTGTTTCGGTTTCTGTTGGTATCGGTATCGCTGCTGCTG
1078  GCCGTGCCGGTCAGCGTCGGGATCGGCATTGCGGCTGCGG

               1130      1140      1150      1160
1121  CTATCGCTTGCGTTGCTGCTGCTGCTGCTGGTGCTTACTT
1158  CGATCGCGTGCGTGGCCGCCGCCGCCGCCGGCGCGTACTT

               1170      1180      1190      1200
1161  CGTTTATATTCGTCGTCGTGGTGCTGGTCCGCTGCCGCGT
1158  CGTCTATACGCGCCGGCGCGGTGCGGGTCCGCTGCCCAGA

               1210      1220      1230      1240
1201  AAACCGAAAAAACTGCCGGCTTTCGGTAACGTTAACTACA
1198  AAGCCAAAAAAGCTGCCGGCCTTTGGCAACGTCAACTACA

               1250
1241  GTGCTCTGCCGGGTTGA
1238  GCGCGCTGCCCGGGTGA
```

FIG. 5

```
                10        20        30        40
  1 MCGPTLAVLGALLAVAVSLPTPAPRVTVYVDPPAYPMPRY
  1 MEGPTLAVLGALLAVAVSLPTPAPRVTVYVDPPAYPMPRY

                50        60        70        80
 41 NYTERWHTTGPIPSPFADGREQPVEVRYATSAAACDMLAL
 41 NYTERWHTTGPIPSPFADGREQPVEVRYATSAAACDMLAL

                90       100       110       120
 81 IADPQVGRTLWEAVRRHARAYNATVIWYKIESGCARPLYY
 81 IADPQVGRTLWEAVRRHARAYNATVIWYKIESGCARPLYY

               130       140       150       160
121 MEYTECEPRKHFGYCRYRTPPFWDSFLAGFAYPTDDELGL
121 MEYTECEPRKHFGYCRYRTPPFWDSFLAGFAYPTDDELGL

               170       180       190       200
161 IXAAPARLVEGQYRRALYIDGTVAYTDFMVSLPAGDCWFS
161 IXAAPARLVEGQYRRALYIDGTVAYTDFMVSLPAFDCWFS

               210       220       230       240
201 KLGAARGYTFGACFPARDYEQKKVLRLTYLTQYYPQEAHK
201 KLGAARGYTFGACFPARDYEQKKVLRLTYLTQYYPQEAHK

               250       260       270       280
241 AIVDYWFMRHGGVVPPYFEESKGYEPPPAADGGSPAPPGD
241 AIVDYWFMRHGGVVPPYFEESKGYEPPPAADGGSPAPPGD

               290       300       310       320
281 DEAREDEGETEDGAAGREGNGGPPGPEGDGESQTPEANGG
281 DEAREDEGETEDGAAGREGNGGPPGPEGDGESQTPEANGG

               330       340       350       360
321 AEGEPKPGPSPDADRPEGWPSLEAITHPPPAPATPA-APD
321 AEGEPKPGPSPDADRPEGWPSLEAITHPPPAPATPARAPD

               370       380       390       400
360 AVPVSVGIGIAAAAIACVAAAAAGAYFVYTRRRGAGPLPR
361 AVSVSVGIGIAAAAIACVAAAAAGAYFVYIRRRGAGPLPR

               410
400 KFKKLPAFGNVNYSALPG *
401 KFKKLPAFGNVNYSALPG *
```

FIG. 6A

```
CTCGAGAAATCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCAATTGTGAGCGGATAACAATT 80
GAGCTCTTTAGTATTTTTTAAATAAACGAAACACTCGCCTATTGTTAATATTATCTAAGTTAACACTCGCCTATTGTTAA

TCACACAGAATTCATTAAAGAGGAGAAATTAACTATGAGAGGATCTCACCATCACCATCACCATACGGATCCGCATGCCA 160
                        6x his:MgD coding seq
AGTGTGTCTTAAGTAATTTCTCCTCTTTAATTGATACTCTCCTAGAGTGGTAGTGGTAGTGGTATGCCTAGGCGTACGGT
                                         6x His leader
                                    Met Arg Gly Ser His His His His His His Asp Pro His Ala
                                                  6x his:MgD coding seq

TGAGCTTGCCTACACCCGCGCCGCGGGTGACGGTATACGTCGACCCGCCGGCGTACCCGATGCCGCGATACAACTACACT 240
ACTCGAACGGATGTGGGCGCGGCGCCCACTGCCATATGCAGCTGGGCGGCCGCATGGGCTACGGCGCTATGTTGATGTGA
                        gD coding sequence
Met Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr
                        6x his:MgD coding seq
GAACGCTGGCACACTACCGGGCCCATACCGTCGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTGCGCTACGCGAC 320
CTTGCGACCGTGTGATGGCCCGGGTATGGCAGCGGGAAGCGTCTGCCGGCGCTCGTCGGGCAGCTCCACGCGATGCGCTG
                        gD coding sequence
Glu Arg Trp His Thr Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val Arg Tyr Ala Thr
                        6x his:MgD coding seq
```

FIG. 6B

```
GAGCGCGGCGGCGTGCGACATGCTGGCGCTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACGCCGGC  400
CTCGCGCCGCCGCACGCTGTACGACCGCGACTAGCGTCTGGGCGTCCACCCCGCGTGCGACACCCTTCGCCATGCGGCCG
                            gD coding sequence
Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg
                            6x his:MgD coding seq

ACGCGCGCGCGTACAACGCCACGGTCATATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTAC  480
TGCGCGCGCGCATGTTGCGGTGCCAGTATACCATGTTCTAGCTCTCGCCCACGCGGGCCGGCGACATGATGTACCTCATG
                            gD coding sequence
His Ala Arg Ala Tyr Asn Ala Tyr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr
                            6x his:MgD coding seq

ACCGAGTGCGAGCCCAGGAAGCACTTTGGGTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTT  560
TGGCTCACGCTCGGGTCCTTCGTGAAACCCATGACGGCGATGGCGTGTGGGGGCAAAACCCTGTCGAAGGACCGCCCGAA
                            gD coding sequence
Thr Glu Cys Glu Pro Arg Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe
                            6x his:MgD coding seq
```

FIG. 6C

```
CGCCTACCCCACGGACGACGAGCTGGGACTGATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACCGACGCGCGC 640
GCGGATGGGGTGCCTGCTGCTCGACCCTGACTAATACCGCCGCGGGCGCGCCGAGCAGCTCCCGGTCATGGCTGCGCGCG
                              gD coding sequence
 Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala
                           6x his:MgD coding seq

TGTACATCGACGGCACGGTCGCCTATACAGATTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCGAAACTCGGC 720
ACATGTAGCTGCCGTGCCAGCGGATATGTCTAAAGTACCAAAGCGACGGCCGGCCCCTGACGACCAAGAGCTTTGAGCCG
                              gD coding sequence
Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly
                           6x his:MgD coding seq

GCGGCTCGCGGGTACACCTTTGGCGCGTGCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACGTATCT 800
CGCCGAGCGCCCATGTGGAAACCGCGCACGAAGGGCCGGGCCCTAATGCTCGTTTTCTTCCAAGACGCGGACTGCATAGA
                              gD coding sequence
 Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu
                           6x his:MgD coding seq

CACGCAGTACTACCCGCAGGAGGCACACAAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGT 880
GTGCGTCATGATGGGCGTCCTCCGTGTGTTCCGGTATCAGCTGATGACCAAGTACGCGGTGCCCCCGCAGCAAGGCGGCA
                              gD coding sequence
 Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro
                           6x his:MgD coding seq

ATTTTGAGGAGTCGAAGGGCTACGAGCCGCCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCC 960
TAAAACTCCTCAGCTTCCCGATGCTCGGCGGCGGACGGCGGCTACCCCCAAGGGGGCGCGGTGGGCCGCTGCTGCTCCGG
                              gD coding sequence
Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala
                           6x his:MgD coding seq
```

FIG. 6D

```
CGCGAGGATGAAGGGGAGACCGAGGACGGGGCAGCCGGGCGGGAGGGCAACGGCGGCCCCCAGGACCCGAAGGCGACGG  1040
GCGCTCCTACTTCCCCTCTGGCTCCTGCCCCGTCGGCCCGCCCTCCCGTTGCCGCCGGGGGTCCTGGGCTTCCGCTGCC
                              gD coding sequence
Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly
                              6x his:MgD coding seq

CGAGAGTCAGACCCCCGAAGCCAACGGAGGCGCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGCCGACCGCCCCG  1120
GCTCTCAGTCTGGGGGCTTCGGTTGCCTCCGCGGCTCCCGCTCGGCTTTGGGCCGGGGTCGGGGCTGCGGCTGGCGGGGC
                              gD coding sequence
Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Aso Arg Pro
                              6x his:MgD coding seq

AAGGCTGGCCGAGCCTCGAAGCCATCACGCACGCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCGGTACCCCGGGTCG  1200
TTCCGACCGGCTCGGAGCTTCGGTAGTGCGTGGGGGCGGGCGGGGGCGATGCGGGCGAGCTCGAGCCATGGGGCCCAGC
                gD coding sequence                        vector coding seq
Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg Ala Arg Tyr Pro Gly Ser
                              6x his:MgD coding seq

ACCTGCAGCCAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTT  1280
TGGACGTCGGTTCGAATTAATCGACTCGAACCTGAGGACAACTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCTAAA
   vector coding seq
Thr Cys Ser Gln Ala *
6x his:MgD coding seq
```

FIG. 7A

CTCGAGAAATCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCAATTGTGAGCGGATAACAATT 80

TCACACAGAATTCATTAAAGAGGAGAAATTAACTATGAGAGGATCTCACCATCACCATCACCATACGGATCCGCATGCCA 160

AGTGTGTCTTAAGTAATTTCTCCTCTTTAATTGATACTCTCCTAGAGTGGTAGTGGTAGTGGTATGCCTAGGCGTACGGT

6X His Leader

Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala

His-LHRH-gD fusion

TGGATCCAGAGCACTGGTCATATGGTCTGCGTCCGGGTGAACATTGGAGCTACGGTCTACGCCCGGGAACACTGGTCT 240

LHRH LHRH LHRH

Met Asp Pro Glu Hrs Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser

His-LHRH-gD fusion

TATGGCTTACGGCCGGGAGAGCATTGGAGTTACGGCCTCCGTCCAGGTTCCATGAGCTTGCCTACACCCGCGCCGCGGGT 320

LHRH LHRH gD coding sequence

Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Ser Met Ser Leu Pro Thr Pro Ala Pro Ala Pro Arg Val

His-LHRH-gD fusion

GACGGTATACGTCGACCCGCCGGCGTACCCGATGCCGCGATACAACTACACTGAACGCTGGCACACTACCGGGCCCATAC 400

gD coding sequence

Thr Val Tyr Cal Asp Pro Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Tro His Thr Thr Gly Pro Ile

His-LHRH-gD fusion

FIG. 7B

CGTCGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTGCGCTACGCGACGAGCGCGGCGGTGCGACATGCTGGCG 480

gD coding sequence

Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala

His-LHRH-gD fusion

CTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACGCCGGCACGCGCGCGTACAACGCCACGGTCAT 560

gD coding sequence

Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala Arg Ala Tyr Asn Ala Thr Val Ile

His-LHRH-gD fusion

ATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTACACCGAGTGCGAGCCCAGGAAGCACTTTG 640

gD coding sequence

Tro Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys His Phe

His-LHRH-gD fusion

GGTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGA 720

gD coding sequence

Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Aso Glu Leu Gly

His-LHRH-gD fusion

CTGATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACCGACGCGCGCTGTACATCGACGGCACGGTCGCCTATAC 800

gD coding sequence

Leu Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr

His-LHRH-gD fusion

FIG. 7C

AGATTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCGAAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGT 880

gD coding sequence

Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala

His-LHRH-gD fusion

GCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACGTATCTCACGCAGTACTACCCGCAGGAGGCACAC 960

gD coding sequence

Cys Phe Pro Ala Arg Asp Tyr Gly Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His

His-LHRH-gD fusion

AAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGTATTTTGAGGAGTCGAAGGGCTACGAGCC 1040

gD coding sequence

Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro

His-LHRH-gD fusion

GCCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACG 1120

gD coding sequence

Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp

His-LHRH-gD fusion

GGGCAGCCGGGCGGGAGGGCAACGGCGGCCCCCAGGACCCGAAGGCGACGGCGAGAGTCAGACCCCCGAAGCCAACGGA 1200

gD coding sequence

Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly

His-LHRH-gD fusion

FIG. 7D

GGCGCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGCCGACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCAC 1280

gD coding sequence

Gly Ala Glu Glu Pro Lys Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly Try Pro Ser Leu Glu Ala Ile Thr

His-gD-LHRH fusion

GCACCCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCGGTACCCCGGGTCGACCTGCAGCCAAGCTTAATTAGCTGAGC 1360

gD coding sequence

vector coding seq

His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg Ala Arg Tyr Pro Gly Ser Thr Cys Ser Gln Ala *

His-gD-LHRH fusion

FIG. 8A

CTCGAGAAATCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCAATTGTGAGCGGATAACAATT 80

TCACACAGAATTCATTAAAGAGGAGAAATTAACTATGAGAGGATCTCACCATCACCATCACCATACGGATCCGCATGCCA 160

6X His Leader

Met Arg Gly Ser His His His His His Thr Asp Pro His Ala

His-gD-LHRH fusion

TGAGCTTGCCTACACCCGCGCCGCGGGTGACGGTATACGTCGACCCGCCGGCGTACCCGATGCCGCGATACAACTACACT 240

mature gD coding seq

Met Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr

His-gD-LHRH fusion

GAACGCTGGCACACTACCGGGCCCATACCGTCGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTGCGCTACGCGAC 320

mature gD coding seq

Glu Arg Trp His Thr Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Arg Tyr Ala Thr

His-gD-LHRH fusion

FIG. 8B

GAGCGCGGCGGCGTGCGACATGCTGGCGCTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACGCCGGC 400

mature gD coding seq

Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg

His-gD-LHRH fusion

ACGCGCGCGTACAACGCCACGGTCATATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTAC 480

mature gD coding seq

His Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr

His-gD-LHRH fusion

ACCGAGTGCGAGCCCAGGAAGCACTTTGGGTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTT 560

mature gD coding seq

Thr Glu Cys Glu Pro Arg Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe

His-gD-LHRH fusion

CGCCTACCCCACGGACGACGAGCTGGGACTGATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACCGACGCGCGC 640

mature gD coding seq

Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala

His-gD-LHRH fusion

TGTACATCGACGGCACGGTCGCCTATACAGATTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCGAAACTCGGC 720

mature gD coding seq

Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly

His-gD-LHRH fusion

FIG. 8C

```
GCGGCTCGCGGGTACACCTTTGGCGCGTGCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACGTATCT  800
                               mature gD coding seq
Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu
                               His-gD-LHRH fusion

CACGCACTACTACCCGCAGGAGGCACACAAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGT  880
                               mature gD coding seq
Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro
                               His-gD-LHRH fusion

ATTTTGAGGAGTCGAAGGGCTACGAGCCGCCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCC  960
                               mature gD coding seq
Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala
                               His-gD-LHRH fusion

CGCGAGGATGAAGGGGAGACCGAGGACGGGGCAGCCGGGCGGGAGGGCAACGGCGGCCCCCCAGGACCCGAAGGCGACGG  1040
                               mature gD coding seq
Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly
                               His-gD-LHRH fusion

CGAGAGTCAGACCCCCGAAGCCAACGGAGGCGCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGCCGACCGCCCCG  1120
                               mature gD coding seq
Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro
                               His-gD-LHRH fusion
```

FIG. 8D

AAGGCTGGCCGAGCCTCGAAGCCATCACGCACCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCCAGAGCACTGGTCA 1200

mature gD coding seq LHRH

Glu Gly Tro Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg Ala Pro Glu His Trp Ser

His-gD-LHRH fusion

TATGGTCTGCGTCCGGGTGAACATTGGAGCTACGGTCTACGCCCCGGGGAACACTGGTCTTATGGCTTACGGCCGGGAGA 1280

LHRH LHRH LHRH

Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu

His-gD-LHRH fusion

GCATTGGAGTTACGGCCTCCGTCCAGGTTGAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACC 1360

LHRH

His Trp Ser Tyr Gly Leu Arg Pro Gly *

His-gD-LHRH fusion

FIG. 9A

```
CTCGAGAAATCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCAATTGTGAGCGGATAACAATT  80

TCACACAGAATTCATTAAAGAGGAGAAATTAACTATGAGAGGATCTCACCATCACCATCACCATACGGATCCGCATGCCA  160
                                    6x His leader
                                    Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala
                                    His-LHRH-gd-LHRH fusion

TGGATCCAGAGCACTGGTCATATGGTCTGCGTCCGGGTGAACATTGGAGCTACGGTCTACGCCCCGGGAACACTGGTCT  240
          LHRH                          LHRH                        LHRH
Met Asp Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser
                         His-LHRH-gd-LHRH fusion

TATGGCTTACGGCCGGGAGAGCATTGGAGTTACGGCCTCCGTCCAGGTTCCATGAGCTTGCCTACACCCGCGCCGCGGGT  320
     LHRH                  LHRH                                  gD coding sequence
Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Ser Met Ser leu Pro Thr Pro Ala Pro Arg Val
                         His-LHRH-gd-LHRH fusion

GACGGTATACGTCGACCCGCCGGCGTACCCGATGCCGCGATACAACTACACTGAACGCTGGCACACTACCGGGCCCATAC  400
                         gD coding sequence
Thr Val Tyr Val Asp Pro Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly Pro Ile
                         His-LHRH-gd-LHRH fusion

CGTCGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGAGGTGCGCTACGCGACGAGCGCGGCGGCGTGCGACATGCTGGCG  480
                         gD coding sequence
Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala
                         His-LHRH-gd-LHRH fusion

CTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACGCCGGCACGCGCGCGCGTACAACGCCACGGTCAT  560
                         gD coding sequence
Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala Arg Ala Tyr Asn Ala Thr Val Ile
                         His-LHRH-gd-LHRH fusion
```

FIG. 9B

ATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTACACCGAGTGCGAGCCCAGGAAGCACTTTG 640

gD coding sequence

Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys Hrs Phe

His-LHRH-gD-LHRH fusion

GGTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGA 720

gD coding sequence

Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly

His-LHRH-gD-LHRH fusion

CTGATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACCGACGCGCGCTGTACATCGACGGCACGGTCGCCTATAC 800

gD coding sequence

Leu Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr

His-LHRH-gD-LHRH fusion

AGATTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCGAAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGT 880

gD coding sequence

Asa Phe Met Val Ser Leu Pro Ala Glv Asa Cys Tro Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala

His-LHRH-gD-LHRH fusion

FIG. 9C

GCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACGTATCTCACGCAGTACTACCCGCAGGAGGCACAC 960

gD coding sequence

Cys Phe Pro Ala Arg Asa Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His

His-LHRH-gD-LHRH fusion

AAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGTATTTTGAGGAGTCGAAGGGCTACGAGCC 1040

CGCAGCAAGGCGGCATAAAACTCCTCAGCTTCCCGATGCTCGG

gD coding sequence

Lys Ala Ile Val Asa Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser Lys Gly Tyr GTlu Pro

His-LHRH-gD-LHRH fusion

GCCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACG 1120

gD coding sequence

Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp

His-LHRH-gD-LHRH fusion

FIG. 9D

GGGCAGCCGGGCGGGAGGGCAACGGCGGCCCCCAGGACCCGAAGGCGACGGCGAGAGTCAGACCCCCGAAGCCAACGGA 1200

gD coding sequence

Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly

His-LHRH-gD-LHRH fusion

GGCGCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCGACGCCGACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCAC 1280

gD coding sequence

Gly Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr

His-LHRH-gD-LHRH fusion

GCACCCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCCAGAGCACTGGTCATATGGTCTGCGTCCGGGTGAACATTGGA 1360

gD coding sequence LHRH LHRH

His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg Ala Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp

His-LHRH-gD-LHRH fusion

GCTACGGTCTACGCCCCGGGGAACACTGGTCTTATGGCTTACGGCCGGGAGAGCATTGGAGTTACGGCCTCCGTCCAGGT 1440

LHRH LHRH LHRH

Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly

His-LHRH-gD-LHRH fusion

FIG. 10

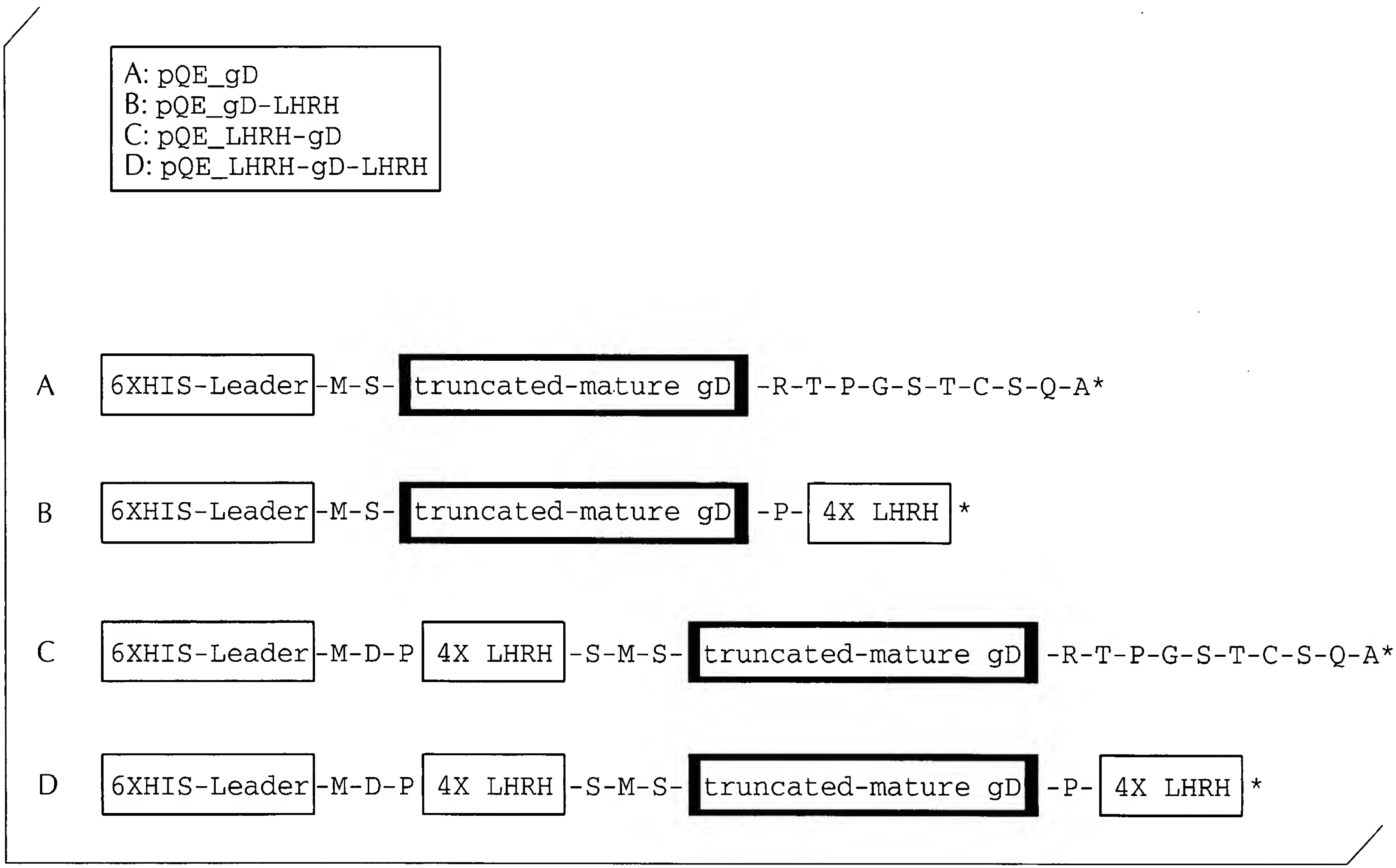

A: pQE_gD
B: pQE_gD-LHRH
C: pQE_LHRH-gD
D: pQE_LHRH-gD-LHRH
A
6XHIS-Leader
-M-S-
truncated-mature gD
-R-T-P-G-S-T-C-S-Q-A*
B
6XHIS-Leader
-M-S-
truncated-mature gD
-P-
4X LHRH
*
C
6XHIS-Leader
-M-D-P
4X LHRH
-S-M-S-
truncated-mature gD
-R-T-P-G-S-T-C-S-Q-A*
D
6XHIS-Leader
-M-D-P
4X LHRH
-S-M-S-
truncated-mature gD
-P-
4X LHRH
*

FIG. 11A

GATATCATGCAGGGGCCGACATTGGCCGTGCTGGGCGCGCTGCTCGCCGTTGCGGTAAGCTTGCCTACACCCGCGCCGCGGGTGACGGTATACGTCGACC 100

signal sequence | Mature gD

Met Gln Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ala Val Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp

gD coding sequence

CGCCGGCGTACCCGATGCCGCGATACAACTACACTGAACGCTGGCACACTACCGGGCCCATACCGTCGCCCTTCGCAGACGGCCGCGAGCAGCCCGTCGA 200

Mature gD

Pro Pro Ala Tyr Pro Met Pro Arg Tyr Asp Tyr Thr Glu Arg Trp His Thr Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu

gD coding sequence

GGTGCGCTACGCGACGAGCGCGGCGGCGTGCGACATGCTGGCGCTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACGCCGGCACGCG 300

Mature gD

Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala

gD coding sequence

CGCGCGTACAACGCCACGGTCATATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTACACCGAGTGCGAGCCCAGGAAGCACT 400

Mature gD

Arg Ala Tyr Asp Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys His

gD coding sequence

FIG. 11B

TTGGGTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGACTGATTATGGCGGCGCC 500

Mature gD

Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro

gD coding sequence

CGCGCGGCTCGTCGAGGGCCAGTACCGACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGATTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGG 600

CGACGGCCGGCCCCTGACGACC

Mature gD

Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp

gD coding sequence

TTCTCGAAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGTGCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACGTATCTCACGC 700

Mature gD

Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu Thr

gD coding sequence

AGTACTACCCGCAGGAGGCACACAAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGTATTTTGAGGAGTCGAAGGGCTACGA 800

Mature gD

Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser Lys Gly Tyr Glu

gD coding sequence

FIG. 11C

GCCGCCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGGCAGCCGGGCGGGAG 900

Mature gD

Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu

gD coding sequence

GGCAACGGCGGCCCCCCAGGACCCGAAGGCGACGGCGAGAGTCAGACCCCCGAAGCCAACGGAGGCGCCGAGGGCGAGCCGAAACCCGGCCCCAGCCCCG 1000

Mature gD

Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro

gD coding sequence

ACGCCGACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCACGCACCCCCCGCCCGCCCCCGCTACGCCCTGAGGTACC 1080

Mature gD

Asp Ala Asp Arg Pro Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro •

gD coding sequence

FIG. 12A

GCGGCCGCAACATATCATGCAGGGGCCGACATTGGCCGTGCTGGGCGCGCTGCTCGCCGTTGCGGTAAGCTTGCCTACACCCGCGCCGCGGGTGACGGTA 100

Signal sequence | Mature gD Sequence

Met Gln Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ala Val Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val

gD-LHRH Coding Sequence

CGTCGACCCGCCGGCGTACCCGATGCCGCGATACAACTACACTGAACGCTGGCACACTACCGGGCCCATACCGTCGCCCTTCGCAGACGGCCGCGAGC 200

Mature gD Sequence

Tyr Val Asp Pro Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu

gD-LHRH Coding Sequence

AGCCCGTCGAGGTGCGCTACGCGACGAGCGCGGCGGCGTGCGACATGCTGGCGCTGATCGCAGACCCGCAGGTGGGGCGCACGCTGTGGGAAGCGGTACG 300

Mature gD Sequence

Gln Pro Val Glu Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln Val Gly Arg Thr Glu Ala Val Arg

gD-LHRH Coding Sequence

CCGGCACGCGCGCGCGTACAACGCCACGGTCATATGGTACAAGATCGAGAGCGGGTGCGCCCGGCCGCTGTACTACATGGAGTACACCGAGTGCGAGCCC 400

Mature gD Sequence

Arg His Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro

gD-LHRH Coding Sequence

AGGAAGCACTTTGGGTACTGCCGCTACCGCACACCCCCGTTTTGGGACAGCTTCCTGGCGGGCTTCGCCTACCCCACGGACGACGAGCTGGGACTGATTA 500

Mature gD Sequence

Arg Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile

gD-LHRH Coding Sequence

TGGCGGCGCCCGCGCGGCTCGTCGAGGGCCAGTACCGACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGATTTCATGGTTTCGCTGCCGGCCGG 600

Mature gD Sequence

Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly

gD-LHRH Coding Sequence

FIG. 12B

GGACTGCTGGTTCTCGAAACTCGGCGCGGCTCGCGGGTACACCTTTGGCGCGTGCTTCCCGGCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCTGACG 700

Mature gD Sequence

p Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr

gD-LHRH Coding Sequence

TATCTCACGCAGTACTACCCGCAGGAGGCACACAAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCGTTCCGCCGTATTTTGAGGAGTCGA 800

Mature gD Sequence

Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser

gD-LHRH Coding Sequence

AGGGCTACGAGCCGCCGCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGGCAGC 900

Mature gD Sequence

Cys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly Ala Ala

gD-LHRH Coding Sequence

CGGGCGGGAGGGCAACGGCGGCCCCCCAGGACCCGAAGGCGACGGCGAGAGTCAGACCCCCGAAGCCAACGGAGGCGCCGAGGGCGAGCCGAAACCCGGC 1000

Mature gD Sequence

ly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro Lys Pro Gly

gD-LHRH Coding Sequence

FIG. 12C

```
CCCAGCCCCGACGCCGACCGCCCCGAAGGCTGGCCGAGCCTCGAAGCCATCACGCACCCCCCGCCCGCCCCCGCTACGCCCGCTCGAGCTCCAGAGCACT  1100
         Mature gD Sequence                                   LHRH
Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg Ala Pro Glu His
                         gD-LHRH Coding Sequence
GGTCATATGGTCTGCGTCCGGGTGAACATTGGAGCTACGGTCTACGCCCCGGGGAACACTGGTCTTATGGCTTACGGCCGGGAGAGCATTGGAGTTACGG  1200
    LHRH            LHRH            LHRH            LHRH
Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly
                         gD-LHRH Coding Sequence

CCTCCGTCCAGGTTGAAGCTGGGATACTAGTGAGCGGCCGC  1241
    LHRH
 Leu Arg Pro Gly  *
 gD-LHRH Coding S
```